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# Microbial diversity of traditional Vietnamese alcohol fermentation starters (*banh men*) as determined by PCR-mediated DGGE

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### Abstract

The diversity of fungi and bacteria associated with traditional Vietnamese alcohol fermentation starters (*banh men*) was investigated by PCR-mediated DGGE. From 52 starter samples, 13 species of fungi (including yeasts) and 23 species of bacteria were identified. The fungal composition of the starters was consistent with little variation among samples. It consisted of amylase producers (*Rhizopus oryzae*, *R. microsporus*, *Absidia corymbifera*, *Amylomyces* sp., *Saccharomycopsis fibuligera*), ethanol producers (*Saccharomyces cerevisiae*, *Issatchenkia* sp., *Pichia anomala*, *Candida tropicalis*, *P. ranongensis*, *Clavispora lusitaniae*), and (opportunistic) contaminants (*Xeromyces bisporus*, *Botryobasidium subcoronatum*). The bacterial microflora of starters was highly variable in species composition and dominated by lactic acid bacteria (LAB). The most abundant LAB were *Lactobacillus* spp. and *Enterococcus* spp.

(LAB). The most frequent LAB were *Pediococcus pentosaceus*, *Lactobacillus plantarum*, *L. brevis*, *Weissella confusa*, and *W. paramesenteroides*. Species of amylase-producing *Bacillus* (*Bacillus subtilis*, *B. circulans*, *B. amyloliquefaciens*, *B. sporothermodurans*), acetic acid bacteria (*Acetobacter orientalis*, *A. pasteurianus*), and plant pathogens/environment contaminants (*Burkholderia ubonensis*, *Ralstonia solanacearum*, *Pelomonas puraquae*) were also detected. Fungal DGGE was found to be useful for evaluating starter type and starter quality. Moreover, in view of the high biological diversity of these substrates, bacterial DGGE may be useful in determining the identity of a starter. The constant occurrence of opportunistic contaminants highlights the need for careful examination of the role of individual components in starters.



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## Keywords

Vietnam; Traditional starter; Alcohol fermentation; *Banh men*; DGGE; Microbial community

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